

Amendments to the Claims:

1-22. (Cancelled)

23. (Withdrawn) A method of ordering pairs of sequence tags, the method comprising the steps of:

- a) providing a population of pairs of sequence tags of restriction fragments, produced by digesting a fragment of genomic DNA with a plurality of combinations of restriction endonucleases;
- b) removing duplicate pairs of sequence tags from the population;
- c) selecting a pair of sequence tags from the population;
- d) comparing each sequence tag of the selected pair with each sequence tag of a first pair and a last pair of a candidate ordering;
- e) adding the selected pair to an end of the candidate ordering whenever a sequence tag of the selected pair matches the sequence tag of the first pair or the last pair of the candidate ordering, to form a new candidate ordering; and
- f) repeating steps c) through e) until all pairs of the population have been selected.

24. (Withdrawn) The method of claim 23, wherein each population of pairs of sequence tags consists of n pluralities of pairs of sequence tags, each plurality being formed by digesting said fragment of genomic DNA in n separate reactions, each with a different n-1 combination of restriction endonucleases, wherein each pair of sequence tags is formed by ligating a portion of each end of each restriction fragment together.

25. (Withdrawn) The method of claim 24, wherein said population of pairs of sequence tags consists of samples of pairs of sequence tags from each of said n pluralities.

26. (Withdrawn) The method of claim 25, wherein each of said samples has the same size.

27. (Withdrawn) The method of claim 26, wherein n =3 and each said restriction endonuclease has a six-basepair recognition site.

28. (Currently amended) A composition comprising a [[A]] plurality of at least 124 different-sequence, same-length oligonucleotides derived from restriction fragments of a polynucleotide,

each said oligonucleotide in the plurality consisting of containing a first end segment and a second end segment[[s]] from opposite ends of one such restriction fragment, wherein

said first end segment consists of a first double stranded end sequence, having 5 to 12 basepairs, immediately adjacent to a single stranded cleaved restriction site;

said second end segment consists of a second double stranded end sequence, having 5 to 12 basepairs, immediately adjacent to a single stranded cleaved restriction site; and

said first end sequence and said second end sequence are ligated attached directly together; and wherein

each end sequence contains the same number of basepairs[[,]] and wherein each end sequence in the plurality of oligonucleotides is unique.

29-33. (Cancelled)